

**Query= SEQ ID NO:1**  
(1509 letters)

Sequences producing significant alignments:

Score (bits)	E Value
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Contig:AC119673.2.1.188119 460 e-126

>Contig:AC119673.2.1.188119  
Length = 188119

Score = 460 bits (232), Expect = e-126  
Identities = 235/236 (99%)  
Strand = Plus / Minus

Query: 255 agtcttcctacagtggcagcaccagcttatccagcatgaagtcgtgaaagagtatag 314  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Sbjct: 172797 agtcttcctacagtggcagcaccagcttatccagcatgaagtcgtgaaagagtatag 172738

Query: 315 ccacctgttcaactatccaaggctcgAACCCAGCTTGCAAGCCTACCTGCTGATGGCTCA 374  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Sbjct: 172737 ccacctgttcaactatccaaggctcgAACCCAGCTTGCAAGCCTACCTGCTGATGGCTCA 172678

Query: 375 ctttgatgtggcctgcCcCCTGAAGAAGGCTGGAGGTGCCcCcATTCTCTGGTTGGA 434  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Sbjct: 172677 ctttgatgtggcctgcCcCCTGAAGAAGGCTGGAGGTGCCcCcATTCTCTGGTTGGA 172618

Query: 435 gcgtgatggcgtcatctatggcgggacactggacgacaagaactctgtgatgg 490  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Sbjct: 172617 gcgtgatggcgtcatctatggcgggacactggacgacaagaactctgtgatgg 172562

Score = 341 bits (172), Expect = 8e-91  
Identities = 172/172 (100%)  
Strand = Plus / Minus

Query: 1114 gaggtcctagaactcacgaagaacattgtggctgataacagagtcacgttccatgtgttg 1173  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Sbjct: 160007 gaggtcctagaactcacgaagaacattgtggctgataacagagtcacgttccatgtgttg 159948

Query: 1174 agtgccttgacCCCTCCCCGTcagccctctgatgacaaggcTTGGCTaccagctg 1233  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Sbjct: 159947 agtgccttgacCCCTCCCCGTcagccctctgatgacaaggcTTGGCTaccagctg 159888

Query: 1234 ctccgccagaccgtacagtccgtttcccggaaagtcaaatattactgccccag 1285  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Sbjct: 159887 ctccgccagaccgtacagtccgtttcccggaaagtcaaatattactgccccag 159836

Score = 341 bits (172), Expect = 8e-91  
Identities = 172/172 (100%)  
Strand = Plus / Minus

Query: 1 atggctcagcggtgcgttgtcgatgctggccctggctatgctgctcctagtttcct 60  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 177310 atggctcagcggtgcgttgtcgatgctggccctggctatgctgctcctagtttcct 177251

Query: 61 accgtctccagatcgatggcccgaggagcgggagcatcaaaggcgctcgcaatccct 120  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 177250 accgtctccagatcgatggcccgaggagcgggagcatcaaaggcgctcgcaatccct 177191

Query: 121 tctcagttcagcaaagaggaacgcgtcgatgaaagaggcgctgaaagg 172  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 177190 tctcagttcagcaaagaggaacgcgtcgatgaaagaggcgctgaaagg 177139

Score = 266 bits (134), Expect = 4e-68  
Identities = 134/134 (100%)  
Strand = Plus / Minus

Query: 575 agtcatcaggcacaggggctcagaggatctcagccctgctacagtcaaggcgcc 634  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 171457 agtcatcaggcacaggggctcagaggatctcagccctgctacagtcaaggcgcc 171398

Query: 635. tagccttcattgtggacgaggggggcttcattctggatgattcattctaactcaaga 694  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 171397 tagccttcattgtggacgaggggggcttcattctggatgattcattctaactcaaga 171338

Query: 695 agcccatgccttg 708  
||||| |||||  
Sbjct: 171337 agcccatgccttg 171324

Score = 248 bits (125), Expect = 9e-63  
Identities = 125/125 (100%)  
Strand = Plus / Minus

Query: 1385 gcatccatggagtcaacgagaaaatctcagtcacgcctatgagaccgaaattca 1444  
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 155447 gcatccatggagtcaacgagaaaatctcagtcacgcctatgagaccgaaattca 155388

Query: 1445 tctttgagttgattcagaatgctgacacagaccaggagccagttctcacctgcacaaac 1504  
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 155387 tctttgagttgattcagaatgctgacacagaccaggagccagttctcacctgcacaaac 155328

Query: 1505 tgtga 1509  
|||||  
Sbjct: 155327 tgtga 155323

Score = 238 bits (120), Expect = 8e-60  
Identities = 120/120 (100%)  
Strand = Plus / Minus

Query: 708 gattgcagtctcagagaagggttccatgaacctcatgctcaagtaaacatgacttcagg 767  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 171024 gattgcagtctcagagaagggttccatgaacctcatgctcaagtaaacatgacttcagg 170965

Query: 768 ccactttcagctcctccaaaggagacaaggcatggcatcctgcagctgctgtcagccg 827  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 170964 ccactttcagctcctccaaaggagacaaggcatggcatcctgcagctgctgtcagccg 170905

Score = 202 bits (102), Expect = 5e-49  
Identities = 102/102 (100%)  
Strand = Plus / Minus

Query: 1284 agttacttctattggcaacacacagacagccgattcttacaaaacctcaccactggcatcta 1343  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 157084 agttacttctattggcaacacacagacagccgattcttacaaaacctcaccactggcatcta 157025

Query: 1344 caggttctacccatctacatacagcctgaagacttcaaacg 1385  
||||||||||||||||||||||||||||||||||||  
Sbjct: 157024 caggttctacccatctacatacagcctgaagacttcaaacg 156983

Score = 178 bits (90), Expect = 7e-42  
Identities = 93/94 (98%)  
Strand = Plus / Minus

Query: 163 ctgaaagggtgccatccagattccaacagtgacttttagctctgagaagtccataactaca 222  
||||||||||||||||||||||||||||||||||||||||  
Sbjct: 175216 ctgacagggtgccatccagattccaacagtgacttttagctctgagaagtccataactaca 175157

Query: 223 gccctggctgagttcgaaaaatacattcataaag 256  
||||||||||||||||||||||||||||||||  
Sbjct: 175156 gccctggctgagttcgaaaaatacattcataaag 175123

Score = 174 bits (88), Expect = 1e-40  
Identities = 88/88 (100%)  
Strand = Plus / Minus

Query: 489 ggcattactgcaggccttggagctcctgctgatcaggaagtacatccccgaagatctt 548  
Sbjct: 172136 ggcattactgcaggccttggagctcctgctgatcaggaagtacatccccgaagatctt 172077

Query: 549 cttcatttctctggccatgtgaggag 576  
Sbjct: 172076 cttcatttctctggccatgtgaggag 172049

Score = 161 bits (81), Expect = 2e-36  
Identities = 81/81 (100%)  
Strand = Plus / Minus

Query: 964 aggttatggagagaaatccctaaccatatgcaataatcaggaccacggcactcacc 1023  
Sbjct: 169129 aggttatggagagaaatccctaaccatatgcaataatcaggaccacggcactcacc 169070

Query: 1024 atattcaaaggcaggggtcaag 1044  
Sbjct: 169069 atattcaaaggcaggggtcaag 169049

Score = 153 bits (77), Expect = 4e-34  
Identities = 77/77 (100%)  
Strand = Plus / Minus

Query: 827 gattggagcagacaccaatgcctatcatatttggaaagcgggacagtggtaactgtattgc 886  
Sbjct: 169990 gattggagcagacaccaatgcctatcatatttggaaagcgggacagtggtaactgtattgc 169931

Query: 887 agcaactggcaaatgag 903  
Sbjct: 169930 agcaactggcaaatgag 169914

Score = 151 bits (76), Expect = 2e-33  
Identities = 76/76 (100%)  
Strand = Plus / Minus

Query: 1043 agttcaatgtcatccccccagtggcccaggccacagtcaacttccggattcaccctggac 1102  
Sbjct: 167563 agttcaatgtcatccccccagtggcccaggccacagtcaacttccggattcaccctggac 167504

Query: 1103 agacagtccaagaggt 1118  
|||||||  
Sbjct: 167503 agacagtccaagaggt 167488

Score = 131 bits (66), Expect = 1e-27  
Identities = 66/66 (100%)  
Strand = Plus / Minus

Query: 902 agtttcccttcctgtcaatataatcctgagcaacccatggctattgaaccacctataa 961  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 169455 agtttcccttcctgtcaatataatcctgagcaacccatggctattgaaccacctataa 169396

Query: 962 gcaggt 967  
|||||  
Sbjct: 169395 gcaggt 169390

**Query=** SEQ ID NO:3  
(1086 letters)

Score (bits)	E Value
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### Sequences producing significant alignments:

Contig:AC119673.2.1.188119 460 e-127

>Contig:AC119673.2.1.188119  
Length = 188119

Score = 460 bits (232), Expect = e-127  
Identities = 235/236 (99%)  
Strand = Plus / Minus

Query: 255 agtcttcctacagtggcagcaccagttatccagcatgaagtcgtgaaagatata 314  
Sbjct: 172797 agtcttcctacagtggcagcaccagttatccagcatgaagtcgtgaaagatata 172738

Query: 315 ccacctgttcaactatccaaaggctcgaccccagttgcagccctacctgctgtatggctca 374  
|||||||  
Sbjct: 172737 ccacctgttcaactatccaaaggctcgaccccagttgcagccctacctgctgtatggctca 172678

Query: 375 ctttgatgtggcgccctgaagaaggctgggaggtgcattctctgggttggaa 434  
||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Sbjct: 172677 ctttgatataatcacctacccctqaqaqaqqctqqqqatgcattctctgggttggaa 172618

Query: 435 gcgtgatggcgtcatctatggtcggggcacactggacgacaagaactctgtatgg 490  
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Sbjct: 172617 gcgtgatggcatcatctatgtcgaaaaacacactggacgacaagaactctgtatgg 172562

Score = 341 bits (172), Expect = 6e-91  
Identities = 172/172 (100%)  
Strand = Plus / Minus

Query: 1 atggctcagcggtgcggttgcgtgctggccctggctatgctgctccatgtttccct 60  
Sbjct: 177310 atggctcagcggtgcggttgcgtgctggccctggctatgctgctccatgtttccct 177251

Query: 61 accgtctccagatcgatggggccgaggagcggggagcatcaaaggcgctgcgaatccct 120  
Sbjct: 177250 accgtctccagatcgatggggccgaggagcggggagcatcaaaggcgctgcgaatccct 177191

Query: 121 tctcagttcgcaaaaggaaacgcgtcgcatgaaagaggcgctgaaagg 172  
|||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 177190 tctcagttcgcaaaaggaaacgcgtcgcatgaaagaggcgctgaaagg 177139

Score = 266 bits (134), Expect = 3e-68  
Identities = 134/134 (100%)  
Strand = Plus / Minus

Query: 575 agtcatcagggacaggggctcagaggatctcagccctgctacagtcaagggcgccagc 634  
|||||||  
Sbjct: 171457 agtcatcagggacaggggctcagaggatctcagccctgctacagtcaagggcgccagc 171398

Query: 635 tagcatttcattgtggacgagggggcttcatcttggatgattcattcctaacttcaaga 694  
|||||||  
Sbjct: 171397 tagcatttcattgtggacgagggggcttcatcttggatgattcattcctaacttcaaga 171338

Query: 695 agcccatgccttg 708  
|||||||  
Sbjct: 171337 agcccatgccttg 171324

Score = 238 bits (120), Expect = 6e-60  
Identities = 120/120 (100%)  
Strand = Plus / Minus

Query: 708 gattgcagtctcagagaagggttccatgaacctcatgctgcaagtaaacatgacttcagg 767  
|||||||  
Sbjct: 171024 gattgcagtctcagagaagggttccatgaacctcatgctgcaagtaaacatgacttcagg 170965

Query: 768 ccactttcagctcctccaaaggagacaaggcatggcatcctgcagctgctgtcagccg 827  
|||||||  
Sbjct: 170964 ccactttcagctcctccaaaggagacaaggcatggcatcctgcagctgctgtcagccg 170905

Score = 178 bits (90), Expect = 5e-42  
Identities = 93/94 (98%)  
Strand = Plus / Minus

Query: 163 ctgaaaagggtgccatccagattccaacagtgacttttagctctgagaagtccaaatactaca 222  
|||||  
Sbjct: 175216 ctgacagggtgccatccagattccaacagtgacttttagctctgagaagtccaaatactaca 175157

Query: 223 gccctggctgagttcgaaaaatacattcataaag 256  
|||||||  
Sbjct: 175156 gccctggctgagttcgaaaaatacattcataaag 175123

Score = 174 bits (88), Expect = 7e-41  
Identities = 88/88 (100%)  
Strand = Plus / Minus

Query: 489 ggcattactgcaggccttggagctcctgctgatcaggaagtacatccccgaagatctt 548  
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 172136 ggcattactgcaggccttggagctcctgctgatcaggaagtacatccccgaagatctt 172077

Query: 549 cttcatttctctggccatgatgaggag 576  
|||||||||||||||||||||||||  
Sbjct: 172076 cttcatttctctggccatgatgaggag 172049

Score = 161 bits (81), Expect = 1e-36  
Identities = 81/81 (100%)  
Strand = Plus / Minus

Query: 902 aggttatggagagaaatccctaaccatatgcaataatcaggaccacggcactcacc 961  
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 169129 aggttatggagagaaatccctaaccatatgcaataatcaggaccacggcactcacc 169070

Query: 962 atattcaaaggcaggggtcaag 982  
|||||||||||||||||  
Sbjct: 169069 atattcaaaggcaggggtcaag 169049

Score = 157 bits (79), Expect = 2e-35  
Identities = 79/79 (100%)  
Strand = Plus / Minus

Query: 827 gattggagcagacaccaatgcctatcatatttggaaagcgggacagtggtaactgtattgc 886  
|||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 169990 gattggagcagacaccaatgcctatcatatttggaaagcgggacagtggtaactgtattgc 169931

Query: 887 agcaactggcaaatgaggt 905  
|||||||||||||||||  
Sbjct: 169930 agcaactggcaaatgaggt 169912

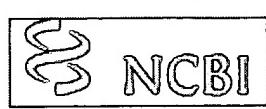
Score = 151 bits (76), Expect = 1e-33  
Identities = 76/76 (100%)  
Strand = Plus / Minus

Query: 981 agttcaatgtcatccccccagtgcccaggccacagtcaacttccggattcaccctggac 1040  
|||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 167563 agttcaatgtcatccccccagtgcccaggccacagtcaacttccggattcaccctggac 167504

Query: 1041 agacagtccaagaggt 1056  
|||||||||||||||  
Sbjct: 167503 agacagtccaagaggt 167488

Score = 69.9 bits (35), Expect = 3e-09  
Identities = 35/35 (100%)  
Strand = Plus / Minus

Query: 1052 gaggtcctagaactcacgaagaacattgtggctga 1086  
|||||||||||||||||||||||||||||||||||||  
Sbjct: 160007 gaggtcctagaactcacgaagaacattgtggctga 159973

 Nucleotide

Entrez PubMed Nucleotide Protein Genome Structure PMC Taxonomy Books

Search  for

Limits Preview/Index History Clipboard Details

Display default Show: 20 Send to File Get Subsequence Features Links

1: AC119673. Homo sapiens chro...[gi:34610310]

LOCUS AC119673 187660 bp DNA linear PRI 13-SEP-2003  
 DEFINITION Homo sapiens chromosome 1 clone RP11-212H11, complete sequence.  
 ACCESSION AC119673 AL365208  
 VERSION AC119673.3 GI:34610310  
 KEYWORDS HTG.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 187660)  
 AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,  
 Saenphimmachak,C., Buckley,D., Kibukawa,M., Raymond,C. and  
 Haugen,E.D.  
 TITLE Direct Submission  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 187660)  
 AUTHORS Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (30-APR-2002) Genome Center, University of Washington,  
 Box 352145, Seattle, WA 98195, USA  
 REFERENCE 3 (bases 1 to 187660)  
 AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,  
 Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.  
 and Haugen,E.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-JUL-2002) Genome Center, University of Washington,  
 Box 352145, Seattle, WA 98195, USA  
 REFERENCE 4 (bases 1 to 187660)  
 AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,  
 Saenphimmachak,C., Buckley,D., Kibukawa,M., Raymond,C. and  
 Haugen,E.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (13-SEP-2003) Genome Center, University of Washington,  
 Box 352145, Seattle, WA 98195, USA  
 COMMENT On Sep 13, 2003 this sequence version replaced gi:21844627.  
 ----- Genome Center  
 Center: University of Washington Genome Center  
 Center Code: UWGC  
 Web site: <http://www.genome.washington.edu>  
 Contact: uwgchtgs@u.washington.edu  
 Drafting Center: SC  
 ----- Project Information  
 Center project name: chr-1  
 Center clone name: RP11-212H11 (sc0653)  
 ----- Summary Statistics  
 Sequencing vector: unknown; 5% of reads  
 Sequencing vector: plasmid; 95% of reads  
 Chemistry: Dye-terminator ET; 43% of reads